CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/720,529

ENTERED

CRF Processing Date: 7/24/2001
Edited by: _____
Verified by: _____ (STIC staff

☐ Changed a file from non-ASCII to ASCII.

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line. *Be*

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: , .
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING   DATE: 07/24/2001
PATENT APPLICATION: US/09/720,529   TIME: 18:10:46

Input Set : **A:\Pto.amc**
Output Set: **N:\CRF3\07242001\I720529.raw**

```
     3 <110> APPLICANT: E. I. du Pont de Nemours and Company
     5 <120> TITLE OF INVENTION: Chromatin Associated Proteins
     7 <130> FILE REFERENCE: BB-1118-A
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/720,529
C--> 10 <141> CURRENT FILING DATE: 2001-06-04
    12 <150> PRIOR APPLICATION NUMBER: 60/092,841
    13 <151> PRIOR FILING DATE: 1998-07-14
    15 <160> NUMBER OF SEQ ID NOS: 8
    17 <170> SOFTWARE: Microsoft Office 97
    19 <210> SEQ ID NO: 1
    20 <211> LENGTH: 1990
    21 <212> TYPE: DNA
    22 <213> ORGANISM: Oryza sativa
    24 <400> SEQUENCE: 1
    25 gctacttcta cgacgcggag gtggggaact actactacgg gcaggggcac ccgatgaagc   60
    26 cgcaccgcat ccggatgacc cacgcgctgc tcgcccacta cggcctcctc gaccagatgc  120
    27 aggtgctcaa gccccacccg gcgcgcgacc gcgacctctg ccgcttccac gccgacgact  180
    28 acgtcgcctt cctccgctcc gtcacgccgg agacccagca ggaccagatc cgggcgctca  240
    29 agcgcttcaa cgtcggcgag gactgccccg tcttcgacgg cctctacagc ttctgccaga  300
    30 cctacgccgg gggatccgtc ggcggcgccg tcaagctcaa ccacggccac gacatcgcca  360
    31 tcaactgggc cggcggcctc caccacgcca agaagtgcga ggcctcggga ttctgctacg  420
    32 tcaacgacat cgtcctcgcc atcctcgagc tcctcaaata ccaccagcgt gttctctatg  480
    33 tggatatcga tatccaccat ggggatggtg tggaggaggc gttctacacg acggacaggg  540
    34 tgatgacggt ctcgttccac aagtttgggg attatttccc ggggaccggg gacattcgcg  600
    35 atattgggca ctcaaagggg aagtattact ctctgaatgt cccgttggac gacggtatcg  660
    36 acgacgagag ctaccagtcg ttgttcaagc cgatcatggg gaaggtgatg gaggttttc   720
    37 gccctggcgc ggtggtgctc cagtgcggtg cggactctct gtcgggtgat aggttgggtt  780
    38 gcttcaacct gtcaatcagg ggccacgcgg aatgcgtgag attcatgagg tccttcaatg  840
    39 tcccgctgtt gctgcttggt ggtggtgggt ataccataag aaatgttgcg cggtgttggt  900
    40 gctatgagac aggagttgca cttggtcatg agctcactga caagatgcct ccaaatgagt  960
    41 attttgagta ctttggtcca gattatacac ttcatgttgc accaagtaac atggagaaca 1020
    42 aaaacacacg ccagcagttg gatgatataa gatcaagact tcttgataat ctttcaaaac 1080
    43 ttcgacatgc tcctagcgtc caatttcaag agcgaccccc tgaggctgag ctacctgagc 1140
    44 aagatgaaga ccaagaggat cctgatgaaa ggcaccatgc tgattctgat gtggaaatgg 1200
    45 atgatgtcaa acctttggat gactcaggaa ggaggagcag tattcagaat gtgagagtta 1260
    46 agagagagtc tgctgaaaca gatgccgcag atcaggatgg taatagggtc gctgcagaga 1320
    47 acaccaaggg cacagaacct gcggctgatg gagttggttc ctcgaaacaa actgttccta 1380
    48 ccgatgcaag tgcgatggcc atagacgaac caggctccct gaaagtcgag ccagataact 1440
    49 caaacaaatt gcaagatcaa ccatcggtgc accagaagac ataatagttc tctctacctt 1500
    50 aaaacttagt aactgatgcc atctatcatc cattgattat attggagaaa ctcccaactt 1560
    51 tgaagcagag agttcatgcc ataccaaaag ttatatacca aatttcgaat ggtatgtaca 1620
    52 cctttcgaac tggtggtgtt ttgtgcaata catttatgcc aggctgacta ttatgtggta 1680
    53 tctattatta gctttagttt aaccctgtct gctgtcgagc aatcggtata gtcgtgcaat 1740
    54 atattctgga tctatcaagc aatgtgagac ggatgtcaaa ccattggttg tgacttcagc 1800
    55 aatgtatgta tatgtaagta tagggacagg cagcaggcgt tactttggtg gaagctacaa 1860
    56 gctttgtctc tcttctcatc cctaatacct acgtggggtg cgtctcgttg ttgtttaggt 1920
    57 attactgcat tcttaaaagt gctcatttag ggtgaaattc taacatcttc taaaaaaaaa 1980
```

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07242001\I720529.raw

```
                                                                   1990
58 aaaaaaaaaa
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 493
62 <212> TYPE: PRT
63 <213> ORGANISM: Oryza sativa
65 <400> SEQUENCE: 2
66 Tyr Phe Tyr Asp Ala Glu Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His
67    1           5                  10                  15
69 Pro Met Lys Pro His Arg Ile Arg Met Thr His Ala Leu Leu Ala His
70              20                  25                  30
72 Tyr Gly Leu Leu Asp Gln Met Gln Val Leu Lys Pro His Pro Ala Arg
73          35                  40                  45
75 Asp Arg Asp Leu Cys Arg Phe His Ala Asp Asp Tyr Val Ala Phe Leu
76      50                  55                  60
78 Arg Ser Val Thr Pro Glu Thr Gln Gln Asp Gln Ile Arg Ala Leu Lys
79 65                  70                  75                  80
81 Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Tyr Ser
82                  85                  90                  95
84 Phe Cys Gln Thr Tyr Ala Gly Gly Ser Val Gly Gly Ala Val Lys Leu
85              100                 105                 110
87 Asn His Gly His Asp Ile Ala Ile Asn Trp Ala Gly Gly Leu His His
88          115                 120                 125
90 Ala Lys Lys Cys Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val
91      130                 135                 140
93 Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Val
94 145                 150                 155                 160
96 Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr
97                  165                 170                 175
99 Thr Asp Arg Val Met Thr Val Ser Phe His Lys Phe Gly Asp Tyr Phe
100                 180                 185                 190
102 Pro Gly Thr Gly Asp Ile Arg Asp Ile Gly His Ser Lys Gly Lys Tyr
103             195                 200                 205
105 Tyr Ser Leu Asn Val Pro Leu Asp Asp Gly Ile Asp Asp Glu Ser Tyr
106     210                 215                 220
108 Gln Ser Leu Phe Lys Pro Ile Met Gly Lys Val Met Glu Val Phe Arg
109 225                 230                 235                 240
111 Pro Gly Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly Asp
112                 245                 250                 255
114 Arg Leu Gly Cys Phe Asn Leu Ser Ile Arg Gly His Ala Glu Cys Val
115             260                 265                 270
117 Arg Phe Met Arg Ser Phe Asn Val Pro Leu Leu Leu Leu Gly Gly Gly
118         275                 280                 285
120 Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Cys Tyr Glu Thr Gly
121     290                 295                 300
123 Val Ala Leu Gly His Glu Leu Thr Asp Lys Met Pro Pro Asn Glu Tyr
124 305                 310                 315                 320
126 Phe Glu Tyr Phe Gly Pro Asp Tyr Thr Leu His Val Ala Pro Ser Asn
127             325                 330                 335
129 Met Glu Asn Lys Asn Thr Arg Gln Gln Leu Asp Asp Ile Arg Ser Arg
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/720,529

DATE: 07/24/2001
TIME: 18:10:46

Input Set : **A:\Pto.amc**
Output Set: **N:\CRF3\07242001\I720529.raw**

```
130                340                345                  350
132 Leu Leu Asp Asn Leu Ser Lys Leu Arg His Ala Pro Ser Val Gln Phe
133         355                360                       365
135 Gln Glu Arg Pro Pro Glu Ala Glu Leu Pro Glu Gln Asp Glu Asp Gln
136     370                375                   380
138 Glu Asp Pro Asp Glu Arg His His Ala Asp Ser Asp Val Glu Met Asp
139 385                390                   395                400
141 Asp Val Lys Pro Leu Asp Asp Ser Gly Arg Arg Ser Ser Ile Gln Asn
142             405                410                    415
144 Val Arg Val Lys Arg Glu Ser Ala Glu Thr Asp Ala Ala Asp Gln Asp
145         420                425                   430
147 Gly Asn Arg Val Ala Ala Glu Asn Thr Lys Gly Thr Glu Pro Ala Ala
148         435                440                   445
150 Asp Gly Val Gly Ser Ser Lys Gln Thr Val Pro Thr Asp Ala Ser Ala
151     450                455                   460
153 Met Ala Ile Asp Glu Pro Gly Ser Leu Lys Val Glu Pro Asp Asn Ser
154 465                470                475                480
156 Asn Lys Leu Gln Asp Gln Pro Ser Val His Gln Lys Thr
157             485                490
```

159 <210> SEQ ID NO: 3
160 <211> LENGTH: 1805
161 <212> TYPE: DNA
162 <213> ORGANISM: Glycine max
164 <400> SEQUENCE: 3

```
165 ctactgcact ctgacactat cagatatcaa tttcagaggc ggactggagg ctggagctgc   60
166 ttcaagtctt caactatctg aatttctgaa ctcatccatt cgttagcgca stagaacgaa  120
167 aactgagtaa tggaaagtgg agggaactcc cttccatcag ggtcagatgg tgtgaagaga  180
168 aaggtttcat atttctatga tccagaggtt ggaaactatt attatgggca gggacaccca  240
169 atgaaaccac acaggattcg aatgacacat gctctttag cccactatgg attgcttcaa  300
170 cacatgcagg ttctgaagcc tatggctgct aaagataggg acctttgcaa gttccatgct  360
171 gatgattatg tggcctttct gagaggcatc accctgaaa cgcagcaaga tcaattgaga  420
172 cagctgaaga ggtttaatgt tggcgaagac tgccctgtat ttgatggtct ttactctttc  480
173 tgccagacat atgcaggagg ttctgttggt ggtgctctaa agttgaacca tggagtatgt  540
174 gatattgcaa taaattgggc tggtggtcta catcatgcaa agaagtgtga ggcttctggg  600
175 ttttgctatg ttaatgacat tgtgctggct attttggaac ttctcaaaat acatgagcgt  660
176 gttctgtatg tggacattga tatccaccat ggtgatggtg tagaggaggc cttttacacc  720
177 accgataggg tcatgactgt ttcgtttcat aagtttgggg attactttcc tggaacaggt  780
178 gatattcgtg atattggata tgctaaaggg aaatattatt cactaaatgt tcccttggat  840
179 gatggaattg atgatgagag ctatcagtcc ttgtttaagc caataatggg aaaggttatg  900
180 gagatttta ggcccggtgc tgttgtatta caatgtggt ctgactcttt atctggggac  960
181 aggttaggtt gtttcaatct ttccataaaa ggtcatgcag agtgtgtcag atatatgaga 1020
182 tcttttaatg ttccccttct attgctcggg ggaggtggct atacaataag aaatgtggca 1080
183 cgttgttggt gtttcgagac tagcgttgct cttgggattg aactagatga taagatgcct 1140
184 caacatgaat attatgaata ttttggtcct gactatactc ttcatgttgc tccaagtaac 1200
185 atggaaaaca agaactcccg acaattattg gatgaaataa gagcaaaact tcttgataat 1260
186 ttatctaggc ttcaacatgc accaagtgtc ccattccagg aacggccacc tgatgcagag 1320
187 cttctagaga gagatgaaga tcaagatgat agagatgaaa gatgggatcc cgattctgac 1380
188 agrgaggttg gcgatgacag caatcctgtt cgcagaaggg tgaaaagtga atgcgttgat 1440
189 gctgaggata aagatacagt gtcggggggtg gactcaatgg cagtggatga accatgcatc 1500
```

RAW SEQUENCE LISTING   DATE: 07/24/2001
PATENT APPLICATION: US/09/720,529   TIME: 18:10:46

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07242001\I720529.raw

```
190 aaagaggagc aggataattt aaaagagctt tctgatcaca ggccaagatg aagcaataat 1560
191 aagcattact gatcaacctt ctccttgact agtgtctgtc gacctgtaaa ttatagtttc 1620
192 ctcctaaagc agtctggcat gcattcatct gacgtctgta gtgtttcaaa tttttgcttt 1680
193 atctggaaac tgaagagata tggtgcaagc ttgccttggc ttttgatgtt tcatattact 1740
194 gcaagatgaa tgtagtagtt attttttctg taaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1800
                                                                    1805
195 aaaaa
197 <210> SEQ ID NO: 4
198 <211> LENGTH: 473
199 <212> TYPE: PRT
200 <213> ORGANISM: Glycine max
202 <400> SEQUENCE: 4
203 Met Glu Ser Gly Gly Asn Ser Leu Pro Ser Gly Ser Asp Gly Val Lys
204  1               5                  10                  15
206 Arg Lys Val Ser Tyr Phe Tyr Asp Pro Glu Val Gly Asn Tyr Tyr Tyr
207             20                  25                  30
209 Gly Gln Gly His Pro Met Lys Pro His Arg Ile Arg Met Thr His Ala
210          35                  40                  45
212 Leu Leu Ala His Tyr Gly Leu Leu Gln His Met Gln Val Leu Lys Pro
213      50                  55                  60
215 Met Ala Ala Lys Asp Arg Asp Leu Cys Lys Phe His Ala Asp Asp Tyr
216  65                  70                  75                  80
218 Val Ala Phe Leu Arg Gly Ile Thr Pro Glu Thr Gln Gln Asp Gln Leu
219              85                  90                  95
221 Arg Gln Leu Lys Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp
222             100                 105                 110
224 Gly Leu Tyr Ser Phe Cys Gln Thr Tyr Ala Gly Gly Ser Val Gly Gly
225             115                 120                 125
227 Ala Leu Lys Leu Asn His Gly Val Cys Asp Ile Ala Ile Asn Trp Ala
228         130                 135                 140
230 Gly Gly Leu His His Ala Lys Lys Cys Glu Ala Ser Gly Phe Cys Tyr
231 145                 150                 155                 160
233 Val Asn Asp Ile Val Leu Ala Ile Leu Glu Leu Leu Lys Ile His Glu
234             165                 170                 175
236 Arg Val Leu Tyr Val Asp Ile Asp Ile His His Gly Asp Gly Val Glu
237             180                 185                 190
239 Glu Ala Phe Tyr Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys
240         195                 200                 205
242 Phe Gly Asp Tyr Phe Pro Gly Thr Gly Asp Ile Arg Asp Ile Gly Tyr
243     210                 215                 220
245 Ala Lys Gly Lys Tyr Tyr Ser Leu Asn Val Pro Leu Asp Asp Gly Ile
246 225                 230                 235                 240
248 Asp Asp Glu Ser Tyr Gln Ser Leu Phe Lys Pro Ile Met Gly Lys Val
249             245                 250                 255
251 Met Glu Ile Phe Arg Pro Gly Ala Val Val Leu Gln Cys Gly Ala Asp
252             260                 265                 270
254 Ser Leu Ser Gly Asp Arg Leu Gly Cys Phe Asn Leu Ser Ile Lys Gly
255         275                 280                 285
257 His Ala Glu Cys Val Arg Tyr Met Arg Ser Phe Asn Val Pro Leu Leu
258     290                 295                 300
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/720,529

DATE: 07/24/2001
TIME: 18:10:46

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07242001\I720529.raw

```
260 Leu Leu Gly Gly Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp
261 305               310               315                   320
263 Cys Phe Glu Thr Ser Val Ala Leu Gly Ile Glu Leu Asp Asp Lys Met
264               325               330                   335
266 Pro Gln His Glu Tyr Tyr Glu Tyr Phe Gly Pro Asp Tyr Thr Leu His
267           340               345               350
269 Val Ala Pro Ser Asn Met Glu Asn Lys Asn Ser Arg Gln Leu Leu Asp
270           355               360               365
272 Glu Ile Arg Ala Lys Leu Leu Asp Asn Leu Ser Arg Leu Gln His Ala
273       370               375               380
275 Pro Ser Val Pro Phe Gln Glu Arg Pro Pro Asp Ala Glu Leu Leu Glu
276 385               390               395                   400
278 Arg Asp Glu Asp Gln Asp Asp Arg Asp Glu Arg Trp Asp Pro Asp Ser
279               405               410               415
281 Asp Arg Glu Val Gly Asp Asp Ser Asn Pro Val Arg Arg Arg Val Lys
282           420               425               430
284 Ser Glu Cys Val Asp Ala Glu Asp Lys Asp Thr Val Ser Gly Val Asp
285           435               440               445
287 Ser Met Ala Val Asp Glu Pro Cys Ile Lys Glu Glu Gln Asp Asn Leu
288       450               455               460
290 Lys Glu Leu Ser Asp His Arg Pro Arg
291 465               470
293 <210> SEQ ID NO: 5
294 <211> LENGTH: 541
295 <212> TYPE: DNA
296 <213> ORGANISM: Triticum aestivum
298 <220> FEATURE:
299 <221> NAME/KEY: unsure
300 <222> LOCATION: (134)
302 <220> FEATURE:
303 <221> NAME/KEY: unsure
304 <222> LOCATION: (387)
306 <220> FEATURE:
307 <221> NAME/KEY: unsure
308 <222> LOCATION: (417)
310 <220> FEATURE:
311 <221> NAME/KEY: unsure
312 <222> LOCATION: (433)
314 <220> FEATURE:
315 <221> NAME/KEY: unsure
316 <222> LOCATION: (464)
318 <220> FEATURE:
319 <221> NAME/KEY: unsure
320 <222> LOCATION: (475)
322 <220> FEATURE:
323 <221> NAME/KEY: unsure
324 <222> LOCATION: (479)
326 <220> FEATURE:
327 <221> NAME/KEY: unsure
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 07/24/2001
PATENT APPLICATION: US/09/720,529   TIME: 18:10:47

         Input Set : **A:\Pto.amc**
         Output Set: **N:\CRF3\07242001\I720529.raw**

```
L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:341 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:345 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:346 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:347 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:371 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:386 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:389 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
```